

REMARKS

The active claims in this case are claims 31 and 37-40.

In the Office Action, it was noted that claims 37 and 38 contain sequences that are not identified by SEQ ID NOs. Claims 37 and 38 are amended to recite a SEQ. ID. NO. in lieu of reciting the actual sequence.

The office action notes that the specification must also identify the SEQ ID NOs. This amendment was earlier provided in Applicant's Response to Notice to Comply and Amendment dated December 20, 2001. See page 2 of the Response where page 52, line 2 and page 53, line 3 of the specification is amended to include reference to SEQ ID NOs. 1 and 2.

A marked up version of the claim amendments is attached. A copy of the Notice to Comply is also attached hereto.

It is believed that no fee is due; however, should any fees under 37 C.F.R. §§ 1.16 to 1.21 be required for any reason, the Commissioner is authorized to deduct said fees from Deposit Account No. 01-2508/11362.0025.DVUS03.

Respectfully submitted,



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MARKED-UP VERSION OF CLAIMS

31. A process for the detection of HIV-3 retrovirus or of its RNA in a biological liquid or tissue, characterized by contacting nucleic acids contained in said biological liquid or tissue with a DNA probe containing at least 360 contiguous sequences corresponding to the genomic RNA of HIV-3 retrovirus under stringent hybridization conditions, washing the hybrid formed with a solution preserving said stringent conditions, and detecting the hybrid formed.

37. The process of claim 31 wherein the DNA probe comprises SEQ. ID. NO: 1 is:

_____10	_____20	_____30	_____40	_____50	_____60
CCC ATGGATT	TGA AGATACA	CATAA AGAAA	TACTG ATGTG	GAAGT TTGAT	AGATC TCTAG
_____70	_____80	_____90	_____100	_____110	_____120
GCA ACACCA	TGT TGCTATG	ATAA CTCACC	CAGAG CTCTT	CCAGA AGGAC	TAAAA ACTGC
_____130	_____140	_____150	_____160	_____170	_____180
TGA CTGAAG	ATTG CTGACA	CTGT GGAAC	TTCC AGCAAA	GACTG CTGAC	ACTGC GGGGA
_____190	_____200	_____210	_____220	_____230	_____240
CTT CCAGTG	GGAG GGACAG	GGGG CGGTT	GGGG AGTGGC	TAACC CTCAG	AAGCT GCATA
_____250	_____260	_____270	_____280	_____290	_____300
TAAG CAGCCG	CTTT CTGCTT	GTACC GGGTC	TCGGT TAGAG	GACC AGGTCT	GAGCC CGGGA
_____310	_____320	_____330	_____340	_____350	_____360
GCTC CCTGGC	CTCT AGCTGA	ACCC GCTCGT	TAAC GCTCAA	TAAAG CTTGC	CTTG AGTGAG

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or the complement thereof.

38. (Amended)The process of claim 31 wherein the DNA probe comprises SEQ. ID. NO: 2 is:

_____10	_____20	_____30	_____40	_____50	_____60
AAC ATGGGAA	ACGC ATTGAG	AAAAG GTAAG	TTTG AGGGAT	GGGC AGCAGT	AAGAG AAAGA
_____70	_____80	_____90	_____100	_____110	_____120
ATG AGAAGAA	CTAG AACCTT	CCCT GAGTCT	GAACC ATGCG	CACCT GAGT	AGGAC AGATC
_____130	_____140	_____150	_____160	_____170	_____180
TCC AGGGAAT	TAGC AGCTAG	AGGAG GGATA	CCAAG TTCCC	ATACT CCTCA	AAACA ATGCA
_____190	_____200	_____210	_____220	_____230	_____240
GCC CTTGCA	TCCT AGAAAG	TCAC CAAGAG	GAAGA AGTAG	GTTTT CCAGT	AGCAC CTCAA
_____250	_____260	_____270	_____280	_____290	_____300
GTG CCTCTAA	GGCC AATGAC	CTATA AAAGGA	GCATT TGACC	TCAG CTTCTT	TTTAA AGAA

310	320	330	340	350	360
AAGGGAGGAC	TGGAAGGGTT	AATTTACTCC	CATAAAAGAG	CAGAAATCCT	GGATCTTTGG

GTGTATAA

or the complement thereof.

39. The process of claim 31 wherein the DNA probe corresponds to the nucleotide sequence coding for proteins p12, p16 or p25 of the HIV-3 retrovirus or the complement thereof.

40. The process of claim 31 wherein the DNA probe corresponds to the nucleotide sequence coding for glycoproteins gp41 or gp120 of the HIV-3 retrovirus or the complement thereof.